



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/687,879  
Source: IFW0  
Date Processed by STIC: 10/5/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~  
~~VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND~~  
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202



IFWO

## RAW SEQUENCE LISTING

DATE: 10/05/2004

PATENT APPLICATION: US/10/687,879

TIME: 10:43:26

Input Set : A:\2428-0125P.ST25.txt

Output Set: N:\CRF4\10052004\J687879.raw

3 <110> APPLICANT: LAMBERT, Bart  
 4 JANSSENS, Stefan  
 5 van AUDENHOVE, Katrien  
 6 PEFEROEN, Marnix  
 8 <120> TITLE OF INVENTION: New Bacillus Thuringiensis Strains and Their Insecticidal  
 9 Proteins  
 11 <130> FILE REFERENCE: 2428-0125P  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/687,879  
 14 <141> CURRENT FILING DATE: 2003-10-20  
 16 <150> PRIOR APPLICATION NUMBER: US 09/220,806  
 17 <151> PRIOR FILING DATE: 1998-12-28  
 19 <150> PRIOR APPLICATION NUMBER: US 08/379,656  
 20 <151> PRIOR FILING DATE: 1995-03-23  
 22 <160> NUMBER OF SEQ ID NOS: 5  
 24 <170> SOFTWARE: PatentIn version 3.2  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 19  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Bacillus thuringiensis  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: misc\_feature  
 34 <222> LOCATION: (1)..(19)  
 35 <223> OTHER INFORMATION: This probe is a part of the coding DNA strand of the cryIG  
 gene,  
 36 described by Smulevitch et al. (1991). This probe is used to  
 37 isolate the bTS02618A gene from its containing strain.  
 39 <400> SEQUENCE: 1 ~  
 40 ttctgtacta ttgattgta 19  
 43 <210> SEQ ID NO: 2  
 44 <211> LENGTH: 1561  
 45 <212> TYPE: DNA  
 46 <213> ORGANISM: Bacillus thuringiensis  
 49 <220> FEATURE:  
 50 <221> NAME/KEY: misc\_feature  
 51 <222> LOCATION: (1)..(1561)  
 52 <223> OTHER INFORMATION: Contains the translation initiation codon of the bTS02618A  
 gene.  
 54 <400> SEQUENCE: 2  
 55 aaaaagaaat aggaataaat actatccatt ttttcaagaa atattttttt attagaaagg 60  
 57 aatcttttctt acacgggaaa atcctaagat tgagagtaaa gatatatata tataaatata 120  
 59 ataaagagtt tgtcaggatt ttgaaagat atgatatgaa catgcactag atttatagta 180  
 61 taggaggaaa aagtatgaat cgaaataatc aaaatgaata tgaaattatt gatgcccccc 240  
 63 attgtgggtg tccatcagat gacgatgtga ggtatccttt ggcaägtgac ccaaatgcag 300  
 65 cgttacaaaa tatgaactat aaagattact tacaaatgac agatgaggac tacactgatt 360

3-4,7

**Does Not Comply  
Corrected Diskette Needed**

67 cttatataaa tcctagttta tctattagtg gtagagatgc agttcagact gcgcttactg 420

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69 ttgttgggag aatactcggg gcttttaggtg ttccgttttc tggacaaata gtgagttttt 480  
 71 atcaattcct tttaaatata ctgtggccag ttaatgatac agctatatgg gaagctttca 540  
 73 tgcgacaggt ggaggaactt gtcaatcaac aaataacaga atttgcaaga aatcaggcac 600  
 75 ttgcaagatt gcaaggatta ggagactctt ttaatgtata tcaacgttcc cttcaaaatt 660  
 W--> 77 **ggttggctga tcgaaatgat acacgaaatt taagtgttgt tctgtcttaa tttatagctt** 720  
 79 tagacottga ttttgtaaat gctattccat tgtttgcagt aaatggacag caggttccat 780  
 81 tactgtcagt atatgcacaa gctgtgaatt tacatttgtt attattaaaa gatgcatttc 840  
 83 tttttggaga aggatgggga ttcacacagg gggaaatttc cacatattat gaccgtcaat 900  
 85 tggaaactaac cgctaagtac actaattact gtgaaacttg gtataatata ggttttagatc 960  
 87 gtitaagagg aacaaatact gaaagtgtgt taagatatca tcaattccgt agagaaatga 1020  
 89 ctttagtggt attagatgtt gtggcgctat ttccatatta tgatgtacga ctttatccaa 1080  
 91 cgggatcaaa cccacagctt acacgtgagg tatatacaga tccgattgta tttaatccac 1140  
 93 cagctaattgt tggactttgc cgacgttggg gtactaatcc ctataatact ttttctgagc 1200  
 95 tcgaaaatgc cttcatcgc ccaccacatc tttttgatag gctgaatagc ttaacaatca 1260  
 97 gcagtaatcg atttccagtt tcatctaatt ttatggatta ttggtcagga catacgttac 1320  
 99 gccgtagtta tctgaacgat tcagcagtac aagaagatag ttatggccta attacaacca 1380  
 101 caagagcaac aattaatccc ggagttgatg gaacaaaccg catagagtca acggcagtag 1440  
 103 attttcgttc tgcattgata ggtatatatg gcgtgaatag agcttctttt gtcccaggag 1500  
 105 gcttgtttta tggtagcact tctcctgcta atggaggatg tagagatctc tatgatacaa 1560  
 107 a 1561  
 110 <210> SEQ ID NO: 3  
 111 <211> LENGTH: 1554  
 112 <212> TYPE: DNA  
 113 <213> ORGANISM: Bacillus thuringiensis  
 116 <220> FEATURE:  
 117 <221> NAME/KEY: misc\_feature  
 118 <222> LOCATION: (1146)..(1148)  
 119 <223> OTHER INFORMATION: Presumed translational stop codon of bTS02618A gene.  
 121 <400> SEQUENCE: 3  
 122 aaaattatcc aacatacatt tatcaaaaag tagatgcacg ggtgttaaag cettatacac 60  
 124 gctatagact agatggattt gtgaagagta gtcaagattt agaaattgat ctcatccacc 120  
 126 atcataaagt ccattcttga aaaaatgtac cagataattt agtatctgat acttactcag 180  
 128 atggttcttg cagcgggaatc aaccgttgtg atgaacagca tcaggtagat atgcagctag 240  
 130 atgcggagca tcatccaatg gattgctgtg aagcggctca aacacatgag ttttcttcc 300  
 132 atattaatac aggggatcta aatgcaagtg tagatcaggg catttgggtt gtattaaaag 360  
 134 ttcgaacaac agatgggtat gcgacgttag gaaatcttga attggttagag gttgggccat 420  
 136 tatcgggtga atctctagaa cgggaacaaa gagataatgc gaaatggaat gcagagctag 480  
 138 gaagaaaacg tgcagaaata gatcgtgtgt atttagctgc gaaacaagca attaatcatc 540  
 140 tgtttgtaga ctatcaagat caacaattaa atccagaaat tgggctagca gaaattaatg 600  
 142 aagcttcaaa tcttgttagag tcaatttcgg gtgtatatag tgatacacta ttacagattc 660  
 144 ctgggattaa ctacgaaatt tacacagagt tatccgatcg cttacaacaa gcacgtatc 720  
 146 tgtatacgtc tagaaatgcg gtgcaaaatg gagactttaa cagtgggtcta gatagttgga 780  
 148 atacaactat ggatgcacg gttcagcaag atggcaatat gcatttctta gttctttcgc 840  
 150 attgggatgc acaagtttcc caacaattga gagtaaatcc gaattgtaag tatgtcttac 900  
 152 gtgtgacagc aagaaaagta ggaggcggag atggatacgt cacaatccga gatggcgctc 960  
 154 atcaccaaga aactcttaca tttaatgcat gtgactacga tgtaaattgt acgtatgtca 1020  
 156 atgacaattc gtatataaca gaagaagtgg tattctaccc agagacaaaa catatgtggg 1080  
 158 tagaggtgag tgaatccgaa ggttcattct atatagacag tattgagttt attgaaacac 1140  
 160 aagagtagaa gagggggatc ctaacgtata gcaactatga gaggatactc cgtacaaaca 1200

see p. 7  
 for env  
 regulation

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162 aagattaaaa aaaggtaaaa tgaatagaac cccctactgg tagaaggacc gataggggggt 1260  
 164 tcttaccatga aaaaatgtag ctgtttacta aggtgtataa aaaacagcat atctgataga 1320  
 166 aaaaagttag taccttataa agaaagaatt ccattcacag ttctcggtatc atataaataa 1380  
 168 tgataggggt atccttctta tttacattat ttttcgcaat tatctcgacg ttcttctttc 1440  
 170 cgctcacaat gatgatgac atgacaacaa tcgcgtccat agcgaactct ttcgatatta 1500  
 172 ataatatcta aactcgtgta gcagtcattt ccattttttt tgatccagta aata 1554

175 &lt;210&gt; SEQ ID NO: 4

176 &lt;211&gt; LENGTH: 4344

177 &lt;212&gt; TYPE: DNA

178 &lt;213&gt; ORGANISM: Bacillus thuringiensis

181 &lt;220&gt; FEATURE:

182 &lt;221&gt; NAME/KEY: CDS

183 &lt;222&gt; LOCATION: (668)..(4141)

184 &lt;223&gt; OTHER INFORMATION: Encompasses the entire sequence of SEQ ID NO:2: from

nucleotide

*↑ move up*

185 position 474 to 2034 in SEQ ID NO:4; also encompasses part of the

186 sequence of SEQ ID NO:3: from nucleotide position 2994 to

187 nucleotide position 4344 in SEQ ID NO:4; SEQ ID NO:3 shows additional

W--> 188 *2207* *2237* nucleotides, located downstream (3') from the sequence shown in

W--&gt; 189 SEQ ID NO:4 (nucleotide position 1352 to nucleotide position 1554 in

W--&gt; 190 SEQ ID NO:3)

192 &lt;400&gt; SEQUENCE: 4

193 gaattcgagc tcggtacett ttcagtgtat cgtttccett ccattcaggtt ttcaaattga 60

195 aaagccgaat gatttgaaac ttgtttacga tgtaagtcatt ttgtctatga cgaaagatac 120

197 gtgtaaaaaa cgtattgaga ttgatgaatg tggacaagta gaaattgact tacaagtatt 180

199 aaagattaag ggtgtccttt cttttatcgg aaatttctct attgaacctt ttctgtgtga 240

201 aaacatgtat acaacgggtg atagagatcc gtctatttcc ttaagtttcc aagatacggg 300

203 atatgtggac catattttaa aatatagcgt ccaacaacta ccattattatg taattgatgg 360

205 tgatcatatt caagtagctg atttacaaat caaactgatg aaagagaatc cgcaatctgc 420

207 tcaagtatca ggtttgtttt gttttgtata tgagtaagaa ccgaagggtt gtaaaaaaga 480

209 aataggaata aatactatcc attttttcaa gaaatatatt tttattagaa aggaatcttt 540

211 cttacacggg aaaatcctaa gattgagagt aaagatatat atatataaat acaataaaga 600

213 gtttgtcagg atttttgaaa gatattgat gaacatgcac tagatttata gtataggagg 660

215 aaaaagt atg aat cga aat aat caa aat gaa tat gaa att att gat gcc 709

216 Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala

217 1 5 10

219 ccc cat tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca 757

220 Pro His Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala

221 15 20 25 30

223 agt gac cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta 805

224 Ser Asp Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu

225 35 40 45

227 caa atg aca gat gag gac tac act gat tct tat ata aat cct agt tta 853

228 Gln Met Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu

229 50 55 60

231 tct att agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg 901

232 Ser Ile Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly

233 65 70 75

235 aga ata ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt 949

236 Arg Ile Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser

*Per 1.823*  
*sequence*  
*rules*

*The*

*<2237*

*response*

*has a*  
*MAXIMUM*  
*of 4 lines.*

*Please*  
*insert a*  
*<2207*  
*after the*  
*fourth line,*  
*and insert*  
*a <2237 at*  
*beginning of*  
*fifth line.*

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237	80						85					90							
239	ttt	tat	caa	ttc	ctt	tta	aat	aca	ctg	tgg	cca	gtt	aat	gat	aca	gct			997
240	Phe	Tyr	Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala			
241	95					100					105					110			
243	ata	tgg	gaa	gct	ttc	atg	cga	cag	gtg	gag	gaa	ctt	gtc	aat	caa	caa			1045
244	Ile	Trp	Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln			
245					115					120					125				
247	ata	aca	gaa	ttt	gca	aga	aat	cag	gca	ctt	gca	aga	ttg	caa	gga	tta			1093
248	Ile	Thr	Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu			
249				130					135				140						
251	gga	gac	tct	ttt	aat	gta	tat	caa	cgt	tcc	ctt	caa	aat	tgg	ttg	gct			1141
252	Gly	Asp	Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala			
253			145					150				155							
255	gat	cga	aat	gat	aca	cga	aat	tta	agt	ggt	ggt	cgt	gct	caa	ttt	ata			1189
256	Asp	Arg	Asn	Asp	Thr	Arg	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile			
257	160					165					170								
259	gct	tta	gac	ctt	gat	ttt	ggt	aat	gct	att	cca	ttg	ttt	gca	gta	aat			1237
260	Ala	Leu	Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn			
261	175					180					185					190			
263	gga	cag	cag	ggt	cca	tta	ctg	tca	gta	tat	gca	caa	gct	gtg	aat	tta			1285
264	Gly	Gln	Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu			
265				195					200						205				
267	cat	ttg	tta	tta	tta	aaa	gat	gca	tct	ctt	ttt	gga	gaa	gga	tgg	gga			1333
268	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly			
269				210					215						220				
271	ttc	aca	cag	ggg	gaa	att	tcc	aca	tat	tat	gac	cgt	caa	ttg	gaa	cta			1381
272	Phe	Thr	Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu			
273			225					230				235							
275	acc	gct	aag	tac	act	aat	tac	tgt	gaa	act	tgg	tat	aat	aca	ggt	tta			1429
276	Thr	Ala	Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu			
277	240					245					250								
279	gat	cgt	tta	aga	gga	aca	aat	act	gaa	agt	tgg	tta	aga	tat	cat	caa			1477
280	Asp	Arg	Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln			
281	255					260					265					270			
283	ttc	cgt	aga	gaa	atg	act	tta</												

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303	aat	agc	tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	1765
304	Asn	Ser	Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	
305					355					360					365		
307	atg	gat	tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	1813
308	Met	Asp	Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	
309				370					375					380			
311	tca	gca	gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	1861
312	Ser	Ala	Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	
313			385						390					395			
315	aca	att	aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	1909
316	Thr	Ile	Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	
317		400					405					410					
319	gta	gat	ttt	cgt	tct	gca	ttg	ata	ggt	ata	tat	ggc	gtg	aat	aga	gct	1957
320	Val	Asp	Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	
321	415				420						425				430		
323	tct	ttt	gtc	cca	gga	ggc	ttg	ttt	aat	ggt	acg	act	tct	cct	gct	aat	2005
324	Ser	Phe	Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	
325				435					440					445			
327	gga	gga	tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	2053
328	Gly	Gly	Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	
329			450						455					460			
331	gaa	agt	acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	gtt	acc	ttt	ttt	2101
332	Glu	Ser	Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	
333			465						470					475			
335	agc	ttt	caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	2149
336	Ser	Phe	Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	
337		480					485					490					
339	cct	act	tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	2197
340	Pro	Thr	Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	
341	495				500						505				510		
343	acc	cca	aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	2245
344	Thr	Pro	Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	
345				515						520				525			
347	gtt	tcg	ggt	act	acg	gtc	tta	aaa	ggt	cca	gga	ttt	aca	gga	ggg	ggt	2293
348	Val	Ser	Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	
349			530						535					540			
351	ata	ctc	cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	gta	acg	2341
352	Ile	Leu	Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	
353			545						550					555			
355	gtt	aat	tca	cca	tta	aca	caa	caa	tat	cgc	cta	aga	gtt	cgt	ttt	gcc	2389
356	Val	Asn	Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	
357		560					565						570				
359	tca	aca	gga	aat	ttc	agt	ata	agg	gta	ctc	cgt	gga	ggg	gtt	tct	atc	2437
360	Ser	Thr	Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	
361	575				580						585				590		
363	ggt	gat	gtt	aga	tta	ggg	agc	aca	atg	aac	aga	ggg	cag	gaa	cta	act	2485
364	Gly	Asp	Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	
365				595						600				605			
367	tac	gaa	tcc	ttt	ttc	aca	aga	gag	ttt	act	act	act	ggt	ccg	ttc	aat	2533

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*error explanation*

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 708



VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:660  
L:188 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:189 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:190 M:259 W: Allowed number of lines exceeded, <223> Other Information: